

3-year course evaluation

Subject: MOL217

Semester and year for completed course evaluation: Course runs Jan-July, written September 2021

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Aim: Describe and justify pedagogical choices in the course, reflect on the student's learning as a result of these choices.

1. SUBJECT DESCRIPTION:

Objectives and Content

The course offers students a thorough training in the use of selected bioinformatic tools for the functional annotation of genes. The course includes projects where students work together. These exercises are based on bioinformatics research in the group of the course instructor. As part of working with the project, students are trained to critically evaluate methods and results. The theme of the projects may vary every year, but at the moment are based on RNA-seq. The course can be part of the Master's program in molecular biology as long as it does not overlap with the content of the master's thesis. It is the supervisor of the master thesis and course coordinator responsible for [MOL217](#) that will together decide if there is an overlap.

Learning Outcomes

The course aims to provide a thorough knowledge about selected bioinformatic tools through case-studies based on experimental data and evaluation of tool performance.

Upon completion of course [MOL217](#), students should be able to:

- explain and discuss the choice of bioinformatics methods that can be used to explore a given problem related to the functional consequence of gene expression data, and use these methods to carry out a project assignment based on independent work and work in groups.
- analyze and discuss results from a major bioinformatics project assignment in the light of own data and data from scientific articles.
- present results and analyzes from a bioinformatics project assignment as a project report.

Required Previous Knowledge

The students should know basic principles of molecular biology ([MOL100](#)+[MOL200](#) or equivalent) and must have passed an introductory course in applied bioinformatics ([MOL204](#) or equivalent).

Recommended Previous Knowledge

[MOL201](#) and MOL203

2. **SUMMARY OF ACTIVITY:** The core of the course is practical bioinformatics tool usage to give students experience in how to employ bioinformatics in a real molecular biology research project. A common challenge faced by many experimental biologists who run large genome-wide experiments is the formidable list of genes in the analysed results. Often papers will only follow up a handful of 'top' genes and the rest remain unexplored. It is important to give students skills on how to interpret them, to the benefit of their research question. We use a recent study (currently RNA-seq based) and students use bioinformatic tools available online (minimal programmatic access) to analyse features of one gene from that list and develop research hypotheses on their possible role in that study.

3. **FOLLOW-UP OF PREVIOUS EVALUATIONS:** I have been responsible for this course in 2019, 2020 and 2021, prior to this, the course was run differently hence there are no previous 3-year evaluations to follow up on. Nevertheless, there are some important points from annual evaluations that are interesting to reflect on:

1. **This course is heavily oversubscribed.** In 2019, the capacity of this course was 5 and was revised to 8; 2019 it was 10 and revised to 12 and 2021 it was 15 and revised to 20 to meet popular demand. In 2019 each student worked individually, and in 2020 and 2021 it was necessary to form groups of 2 or 3 per project topic. This has had largely positive effects in terms of inclusivity, as well as team-work experience gained through co-working. The students seem to enjoy this aspect, and we have not had concerns regarding mis-match of work put in by group members. We have discussed with students their opinions regarding our current model of project based bioinformatics with thesis type report versus bioinformatics lectures and practicals with exam, as the latter would allow us to offer it to more students. They overwhelmingly support the current model rather than lectures+practicals. If converted to a lecture course, it would have large overlap with BINF201 and BINF301. Those are poorly subscribed and a merger might be considered to help with our waiting lists.

2. **Active student participation:** This course uses data from a recently published paper or active study from my research group and Mol217 students receive an introduction to the broader research problem, and then are free to choose a gene from the final output list that they will work on for the rest of the course. They are supported in making this choice by the instructors, and must justify this choice before we agree on its selection and in the final report. The students find this very challenging and it stretches them but once they have settled on a gene they are extremely motivated to explore different methods, read primary literature, discuss and get to know everything about 'their' gene. Observing this commitment being developed is extremely motivating for the instructors as well.

3. **Heavy load.** Most students experience that the work-load in the course is somewhat large in relation to the scope of 10 ECTS. Comments on this from the students indicate that: It can be difficult to balance this subject with other subjects. The course involves a lot of work in a short time, and when students get 'stuck' there is not much immediate help and they must wait for the next weekly session. There is generally positive feedback on guidance and availability of instructors when they appreciate that 10 research projects are run by one

instructor and 1-2 junior TAs. Students who have completed the course often feel very motivated towards a career in research.

3. Corona Situation:

All lectures/ help sessions moved online, and students had flexible hours with instructors, which was helpful during lockdown. Students got more support as a result, but it took more effort from instructors as it became common for each group to expect an hour rather than the in-person standard of all groups present for 3h per week. If we undertake this course online again, we will use the online break-out rooms more efficiently, with instructors moving between virtual rooms.

In 2019, the evaluation consisted of Report and oral presentation. The oral presentation was challenging to administer, requiring an external evaluator for several hours. The corona situation and rising student numbers necessitating joint working meant that we cancelled this and moved to evaluating written reports: Part A: report of joint working, jointly assessed and group members get the same mark. Part B: Introduction/ conclusion /discussion on the project carried out which is individually completed and assessed. This has worked very well, with talented students getting better marks within the same group.

Experiences from others who contribute to the teaching of the course, both students and staff Currently there is one supervisor (myself) overseeing 10 projects with the help of 1-2 TAs. A consistent issue has been that the students' demand to always have sessions with me rather than the TAs, which is not practical. The reason for this is that the TAs are experienced in the technical aspects but not the scientific/ research aspect. In the future we will explore if other supervisors might like to suggest their own lab studies/ favourite genes, in analogy to MOL231 for example, so that they can extend the academic support needed to students working on their gene/ pathway by discussing their results with them periodically.

The failure rate on the course

Once we have a stable number of registered students, about 10% drop off, some have taken too many credits and this course is demanding in time. Others leave the course as they find it too difficult to follow the active student-driven learning model and prefer to know exactly what to do in advance. Of the students who completed the course, there have been no fail marks and there is a good distribution of grades from A-D.

Possible peer review

Assessment of correspondence between the course's learning outcome description and teaching, learning and assessment methods: There seems to be a good match between the learning outcome description and teaching, learning and assessment methods. The practical training in bioinformatics analysis as well as the partially independent work with records and presentation of this as thesis provides a total good coverage of the learning objectives.

Assessment of whether progress and arrangements for the course are in accordance with the established goals for the course and program

Progress and arrangements for the course are mainly in accordance with set goals.